

SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
Nehls, Michael
Friedrich, Glenn
Scoville, John
Zambrowicz, Brian
Sands, Arthur T.

<120> Novel Human 7TM Proteins and Receptors and
Polynucleotides Encoding the Same

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<151> 1999-09-10

<150> US 60/165,510
<151> 1999-11-15

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Pro Ser Thr Thr Pro Pro Thr Val Thr Asn Met Pro Val Thr Asn			
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Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu Asp Lys Ile			

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Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln Pro Ser Glu Tyr		
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Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr		
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Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser Thr Ser His Val		
660	665	670
Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser Ser Leu Leu Pro		
675	680	685
Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu Pro Ser Asn Asn		
690	695	700
Glu Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu		
705	710	715
Ala Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu		
725	730	735
Asp Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr		
740	745	750
Gly Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr		
755	760	765
Val Met Ala Cys Ser Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp		
770	775	780
Pro Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln Glu Val His His		
785	790	795
Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly		
805	810	815
Trp Asn Thr Ser Gly Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu		
820	825	830
Thr Val Cys Leu Cys Asn His Phe Thr His Phe Gly Val Leu Met Asp		
835	840	845
Leu Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu		
850	855	860
Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala		
865	870	875
Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr		
885	890	895
Pro Ser Lys Ile Leu Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn		

900	905	910
Leu Leu Phe Leu Leu Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly		
915	920	925
Leu Cys Ile Ala Val Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr		
930	935	940
Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val		
945	950	955
Lys Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile		
965	970	975
Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val Val Leu Ala Ser		
980	985	990
Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys		
995	1000	1005
Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr		
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Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe		
1025	1030	1035
Ile Val Val Met Val Glu Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn		
1045	1050	1055
Arg Thr Leu Arg Glu Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser		
1060	1065	1070
Leu Thr Phe Leu Leu Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp		
1075	1080	1085
Gly Pro Leu Asn Ile Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser		
1090	1095	1100
Leu Gln Gly Leu Phe Ile Phe Ile Phe His Cys Ala Met Lys Glu Asn		
1105	1110	1115
Val Gln Lys Gln Trp Arg Arg His Leu Cys Cys Gly Arg Phe Arg Leu		
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Ala Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys		
1140	1145	1150
Ser Ser Asp Asn Leu Gly Lys Ser Leu Ser Ser Ser Ile Gly Ser		
1155	1160	1165
Asn Ser Thr Tyr Leu Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr		
1170	1175	1180
Phe Lys Arg Asn Ser His Thr Asp Asn Val Ser Tyr Glu His Ser Phe		
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Asn Lys Ser Gly Ser Leu Arg Gln Cys Phe His Gly Gln Val Leu Val		
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Lys Thr Gly Pro Cys		
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cttgcataatg gagagagcca gactaaattt tgtggagcaa ctgccaaagg cctatcattt	360
aactcaatgt cgaatgagat gcatgtgtcc ttttcaatgt acttttagcat ccagaagaaa	420
gtttcaatgt ccagctacat cagagttgcc gtgtccttaa ggaatcaaaa ggtcatttta	480

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<212> PRT
<213> homo sapiens

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35 40 45
Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
50 55 60
Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln
65 70 75 80
Ile Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr
85 90 95
Asp Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly
100 105 110
Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His
115 120 125
Val Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala
130 135 140
Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu
145 150 155 160
Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser

165	170	175
Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val		
180	185	190
Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser		
195	200	205
Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu		
210	215	220
Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys		
225	230	235
Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val		
245	250	255
Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr		
260	265	270
Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn		
275	280	285
Gly Lys Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys		
290	295	300
Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys		
305	310	315
Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp		
325	330	335
Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser		
340	345	350
Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu		
355	360	365
Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Ala Thr Val Asn Ser		
370	375	380
Pro Ser Thr Thr Pro Pro Thr Val Thr Asn Met Pro Val Thr Asn		
385	390	395
Arg Ile Asp Lys Gln Arg Asn Asp Gly Ile Ile Tyr Arg Ile Ser Val		
405	410	415
Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val Gln Ser Lys		
420	425	430
Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn Tyr Thr Val		
435	440	445
Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu Asp Lys Ile		
450	455	460
Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val Leu Trp Ala		
465	470	475
Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu Glu Gly Lys Ile		
485	490	495
Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu Asp Glu Gly Leu		
500	505	510
Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His Cys Leu Ala Met		
515	520	525
Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln Pro Ser Glu Tyr		
530	535	540
Val Leu Pro Cys Pro Asp Lys Pro Gly Phe Ser Ala Ser Arg Ile Cys		
545	550	555
Phe Tyr Asn Ala Thr Asn Pro Leu Val Thr Tyr Trp Gly Pro Val Asp		
565	570	575
Ile Ser Asn Cys Leu Lys Glu Ala Asn Glu Val Ala Asn Gln Ile Leu		
580	585	590
Asn Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala Asn Ile Thr Asn		
595	600	605
Ile Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu Glu Asn Ile Asp		

610	615	620
Ile Thr Leu Gly Ser Thr	Leu Met Asn Ile Phe Ser Asn Ile Leu Ser	
625	630	640
Ser Ser Asp Ser Asp	Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr	
645	650	655
Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser Thr Ser His Val		
660	665	670
Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser Ser Leu Leu Pro		
675	680	685
Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu Pro Ser Asn Asn		
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Glu Ser Tyr Phe Gln Val Met Ser Gln Trp Phe Leu Ser Phe		
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<211> 1112

<212> PRT

<213> homo sapiens

<400> 8

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										20		25			30
Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
										35		40			45
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
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Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
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Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
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Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
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Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
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Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
										130		135			140
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
										145		150			160
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
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Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
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Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
										195		200			205
Phe	Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu
										210		215			220
Ser	Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys

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Trp	Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr
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Glu	Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn
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Gly	Lys	Leu	Leu	Leu	Gly	Ser	Asn	Gln	Asn	Glu	Ile	Val	Ser	Leu	Lys
290								295						300	
Gly	Asp	Ile	Tyr	Asn	Phe	Arg	Leu	Trp	Asn	Phe	Thr	Met	Asn	Ala	Lys
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Ile	Leu	Ser	Asn	Leu	Ser	Cys	Asn	Val	Lys	Gly	Asn	Val	Val	Asp	Trp
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Gln	Asn	Asp	Phe	Trp	Asn	Ile	Pro	Asn	Leu	Ala	Leu	Lys	Ala	Glu	Ser
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Asn	Leu	Ser	Cys	Gly	Ser	Tyr	Leu	Ile	Pro	Leu	Pro	Ala	Ala	Glu	Leu
								355						360	
Ala	Ser	Cys	Ala	Asp	Leu	Gly	Thr	Leu	Cys	Gln	Ala	Thr	Val	Asn	Ser
								370						375	
Pro	Ser	Thr	Thr	Pro	Pro	Thr	Val	Thr	Thr	Asn	Met	Pro	Val	Thr	Asn
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Arg	Ile	Asp	Lys	Gln	Arg	Asn	Asp	Gly	Ile	Ile	Tyr	Arg	Ile	Ser	Val
								405						410	
Val	Ile	Gln	Asn	Ile	Leu	Arg	His	Pro	Glu	Val	Lys	Val	Gln	Ser	Lys
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Val	Ala	Glu	Trp	Leu	Asn	Ser	Thr	Phe	Gln	Asn	Trp	Asn	Tyr	Thr	Val
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Tyr	Val	Val	Asn	Ile	Ser	Phe	His	Leu	Ser	Ala	Gly	Glu	Asp	Lys	Ile
								450						455	
Lys	Val	Lys	Arg	Ser	Leu	Glu	Asp	Glu	Pro	Arg	Leu	Val	Leu	Trp	Ala
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Leu	Leu	Val	Tyr	Asn	Ala	Thr	Asn	Asn	Thr	Asn	Leu	Glu	Gly	Lys	Ile
								485						490	
Ile	Gln	Gln	Lys	Leu	Leu	Lys	Asn	Asn	Glu	Ser	Leu	Asp	Glu	Gly	Leu
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Arg	Leu	His	Thr	Val	Asn	Val	Arg	Gln	Leu	Gly	His	Cys	Leu	Ala	Met
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Glu	Glu	Pro	Lys	Gly	Tyr	Tyr	Trp	Pro	Ser	Ile	Gln	Pro	Ser	Glu	Tyr
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Val	Leu	Pro	Cys	Pro	Asp	Lys	Pro	Gly	Phe	Ser	Ala	Ser	Arg	Ile	Cys
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Phe	Tyr	Asn	Ala	Thr	Asn	Pro	Leu	Val	Thr	Tyr	Trp	Gly	Pro	Val	Asp
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Ile	Ser	Asn	Cys	Leu	Lys	Glu	Ala	Asn	Glu	Val	Ala	Asn	Gln	Ile	Leu
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Asn	Leu	Thr	Ala	Asp	Gly	Gln	Asn	Leu	Thr	Ser	Ala	Asn	Ile	Thr	Asn
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Ile	Val	Glu	Gln	Val	Lys	Arg	Ile	Val	Asn	Lys	Glu	Glu	Asn	Ile	Asp
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								625						630	
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Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu Pro Ser Asn Asn		
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Glu Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu		
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Ala Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu		720
725	730	735
Asp Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr		
740	745	750
Gly Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr		
755	760	765
Val Met Ala Cys Ser Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp		
770	775	780
Pro Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln Glu Val His His		
785	790	795
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Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly		
805	810	815
Trp Asn Thr Ser Gly Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu		
820	825	830
Thr Val Cys Leu Cys Asn His Phe Thr His Phe Gly Val Leu Met Asp		
835	840	845
Leu Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu		
850	855	860
Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala		
865	870	875
880		
Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr		
885	890	895
Pro Ser Lys Ile Leu Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn		
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Leu Leu Phe Leu Leu Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly		
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Leu Cys Ile Aia Val Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr		
930	935	940
Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val		
945	950	955
960		
Lys Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile		
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Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val Val Leu Ala Ser		
980	985	990
Arg Asn Asn Asn Glu Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys		
995	1000	1005
Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr		
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Cys Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe		
1025	1030	1035
1040		
Ile Val Val Met Val Gln Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn		
1045	1050	1055
Arg Thr Leu Arg Glu Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser		
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Leu Thr Phe Leu Leu Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp		
1075	1080	1085
Gly Pro Leu Asn Ile Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser		
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<212> PRT

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								20			25			30		
Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro	Ser	
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Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser	Gln	
								50			55			60		
Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln	Ile	
								65			70			75		80
Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr	Asp	
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Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly	Ala	
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Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His	Val	
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Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala	Ser	
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Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu	Pro	
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Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	Ile	
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Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	Gly	
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His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	Phe	
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Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	Trp	
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Thr	Val	Pro	Cys	Asp	Ser	Thr	Ile	Ser	Lys	Val	Ile	Pro	Gly	Asn	Gly	
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 Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser Asn
 340 345 350
 Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu Ala
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 Ser Thr Thr Pro Pro Thr Val Thr Asn Met Pro Val Thr Asn Arg
 Ile Asp Lys Gln Arg Asn Asp Gly Ile Ile Tyr Arg Ile Ser Val Val
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 Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val Gln Ser Lys Val
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 Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn Tyr Thr Val Tyr
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 450 455 460
 Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val Leu Trp Ala Leu
 465 470 475 480
 Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu Glu Gly Lys Ile Ile
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 Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu Asp Glu Gly Leu Arg
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 Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala Asn Ile Thr Asn Ile
 595 600 605
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 Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser Asn Ile Leu Ser Ser
 625 630 635 640
 Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr Ile
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 Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser Thr Ser His Val Asn
 660 665 670
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 Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu Ala
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 Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu Asp
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Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe Asn Lys Thr Gly
 740 745 750
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 755 760 765
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 Val Cys Leu Cys Asn His Phe Thr His Phe Gly Val Leu Met Asp Leu
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 Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu Thr
 850 855 860
 Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala Ala
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 Ser Lys Ile Leu Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn Leu
 900 905 910
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 Gln Lys Gln Trp Arg Arg His Leu Cys Cys Gly Arg Phe Arg Leu Ala
 1125 1130 1135
 Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys Ser
 1140 1145 1150
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gaa	agttat	g	gaa	agaaa	aaa	agg	ataat	3060
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tga								3663

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<212> PRT

<213> homo sapiens

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Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro	Ser
									35			40		45	
Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser	Gln
									50			55		60	
Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln	Ile
									65			70		75	80
Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr	Asp
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Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly	Ala
									100			105		110	
Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His	Val
									115			120		125	
Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala	Ser
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Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu	Pro
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Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	Ile
									165			170		175	
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 225 230 235 240
 Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val Trp
 245 250 255
 Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr Glu
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 Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn Gly
 275 280 285
 Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys Gly
 290 295 300
 Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys Ile
 305 310 315 320
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 325 330 335
 Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser Asn
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 370 375 380
 Ser Thr Thr Pro Pro Thr Val Thr Thr Asn Met Pro Val Thr Asn Arg
 385 390 395 400
 Ile Asp Lys Gln Arg Asn Asp Gly Ile Ile Tyr Arg Ile Ser Val Val
 405 410 415
 Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val Gln Ser Lys Val
 420 425 430
 Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn Tyr Thr Val Tyr
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 Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu Asp Lys Ile Lys
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 Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val Leu Trp Ala Leu
 465 470 475 480
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 485 490 495
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 580 585 590
 Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala Asn Ile Thr Asn Ile
 595 600 605
 Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu Glu Asn Ile Asp Ile
 610 615 620
 Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser Asn Ile Leu Ser Ser
 625 630 635 640
 Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr Ile
 645 650 655

Asp	Glu	Leu	Ala	Phe	Lys	Ile	Asp	Leu	Asn	Ser	Thr	Ser	His	Val	Asn
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Ile	Thr	Thr	Arg	Asn	Leu	Ala	Leu	Ser	Val	Ser	Ser	Leu	Leu	Pro	Gly
							675		680						685
Thr	Asn	Ala	Ile	Ser	Asn	Phe	Ser	Ile	Gly	Leu	Pro	Ser	Asn	Asn	Glu
							690		695						700
Ser	Tyr	Phe	Gln	Met	Asp	Phe	Glu	Ser	Gly	Gln	Val	Asp	Pro	Leu	Ala
							705		710		715				720
Ser	Val	Ile	Leu	Pro	Pro	Asn	Leu	Leu	Glu	Asn	Leu	Ser	Pro	Glu	Asp
							725		730						735
Ser	Val	Leu	Val	Arg	Arg	Ala	Gln	Phe	Thr	Phe	Phe	Asn	Lys	Thr	Gly
							740		745						750
Leu	Phe	Gln	Asp	Val	Gly	Pro	Gln	Arg	Lys	Thr	Leu	Val	Ser	Tyr	Val
							755		760						765
Met	Ala	Cys	Ser	Ile	Gly	Asn	Ile	Thr	Ile	Gln	Asn	Leu	Lys	Asp	Pro
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Val	Gln	Ile	Lys	Ile	Lys	His	Thr	Arg	Thr	Gln	Glu	Val	His	His	Pro
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Ile	Cys	Ala	Phe	Trp	Asp	Leu	Asn	Lys	Asn	Lys	Ser	Phe	Gly	Gly	Trp
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Asn	Thr	Ser	Gly	Cys	Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr
							820		825						830
Val	Cys	Leu	Cys	Asn	His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Asp	Leu
							835		840						845
Pro	Arg	Ser	Ala	Ser	Gln	Leu	Asp	Ala	Arg	Asn	Thr	Lys	Val	Leu	Thr
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Phe	Ile	Ser	Tyr	Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	Ser	Ala	Ala
							865		870		875				880
Thr	Leu	Leu	Thr	Tyr	Val	Ala	Phe	Glu	Lys	Leu	Arg	Arg	Asp	Tyr	Pro
							885		890		895				900
Ser	Lys	Ile	Leu	Met	Asn	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu
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Leu	Phe	Leu	Leu	Asp	Gly	Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly	Leu
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Cys	Ile	Ala	Val	Ala	Val	Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe
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Thr	Trp	Met	Gly	Leu	Glu	Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys
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Val	Phe	Asn	Thr	Tyr	Ile	Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile
							965		970						975
Gly	Trp	Gly	Leu	Pro	Ala	Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg
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Asn	Asn	Asn	Glu	Val	Tyr	Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly
							995		1000						1005
Asp	Glu	Phe	Cys	Trp	Ile	Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr	Cys
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Val	Val	Met	Val	Gln	Ile	Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg
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Ser Asp Asn Leu Gly Lys Ser Leu Ser Ser Ser Ile Gly Ser Asn
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Ser Thr Tyr Leu Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr Phe
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Lys Arg Asn Ser His Thr Asp Asn Val Ser Tyr Glu His Ser Phe Asn
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885	890	895
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Cys Ile Ala Val Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr Phe		
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Val Phe Asn Thr Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile		
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Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr Cys		
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Ala Gly Tyr Phe Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe Ile		
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<213> homo sapiens

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 Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His
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 Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser
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 Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser
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 Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu
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 Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn
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 Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys
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 Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser
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<212> PRT

<213> homo sapiens

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Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
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Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln
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Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His
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Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu
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Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser
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Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser
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385 390 395 400
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<210> 22

<211> 718

<212> PRT

<213> homo sapiens

<400> 22

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His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
							65		70			75			80
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
							85		90			95			
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 Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser
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 Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val
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 Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser
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<211> 3339

<212> DNA

<213> homo sapiens

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<211> 1112

<212> PRT

<213> homo sapiens

<400> 24

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							20			25		30			
His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
							50			55		60			
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
							65			70		75			80
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
							85			90		95			
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Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
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 225 230 235 240
 Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val
 245 250 255
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 Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn
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 Gly Lys Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys
 290 295 300
 Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys
 305 310 315 320
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 325 330 335
 Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser
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 385 390 395 400
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 420 425 430
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 Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val Leu Trp Ala
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Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala Leu Lys Thr
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 Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu Pro Ser Asn Asn
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 Pro Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln Glu Val His His
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<211> 1626

<212> DNA

<213> homo sapiens

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<211> 541

<312> PRT

<213> homo sapiens

<400> 26

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Arg	Arg	Ala	Gln	Phe	Thr	Phe	Phe	Asn	Lys	Thr	Gly	Leu	Phe	Gln	Asp
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Val	Gly	Pro	Gln	Arg	Lys	Thr	Leu	Val	Ser	Tyr	Val	Met	Ala	Cys	Ser
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 Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly Trp Asn Thr Ser Gly
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 Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu Thr Val Cys Leu Cys
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 Asn His Phe Thr His Phe Gly Val Leu Met Asp Leu Pro Arg Ser Ala
 130 135 140
 Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu Thr Phe Ile Ser Tyr
 145 150 155 160
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 Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr Pro Ser Lys Ile Leu
 180 185 190
 Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn Leu Leu Phe Leu Leu
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 Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly Leu Cys Ile Ala Val
 210 215 220
 Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr Phe Thr Trp Met Gly
 225 230 235 240
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 245 250 255
 Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile Gly Trp Gly Leu
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 370 375 380
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 420 425 430
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 Gly Lys Ser Leu Ser Ser Ser Ile Gly Ser Asn Ser Thr Tyr Leu
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 Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr Phe Lys Arg Asn Ser
 465 470 475 480
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 485 490 495
 Ala Asp Gly Asp Gln Thr Ser Ile Ile Pro Val His Gln Val Ile Asp
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 Lys Val Lys Gly Tyr Cys Asn Ala His Ser Asp Asn Phe Tyr Lys Asn
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<212> DNA

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Val	Gly	Pro	Gln	Arg	Lys	Thr	Leu	Val	Ser	Tyr	Val	Met	Ala	Cys	Ser		
														50	55	60	
Ile	Gly	Asn	Ile	Thr	Ile	Gln	Asn	Leu	Lys	Asp	Pro	Val	Gln	Ile	Lys		
														65	70	75	80
Ile	Lys	His	Thr	Arg	Thr	Gln	Glu	Val	His	His	Pro	Ile	Cys	Ala	Phe		
														85	90	95	
Trp	Asp	Leu	Asn	Lys	Asn	Ser	Phe	Gly	Gly	Trp	Asn	Thr	Ser	Gly			
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 Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu Thr Phe Ile Ser Tyr
 145 150 155 160
 Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala Ala Thr Leu Leu Thr
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 Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr Pro Ser Lys Ile Leu
 180 185 190
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 210 215 220
 Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr Phe Thr Trp Met Gly
 225 230 235 240
 Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val Lys Val Phe Asn Thr
 245 250 255
 Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile Gly Trp Gly Leu
 260 265 270
 Pro Ala Leu Val Val Ser Val Val Leu Ala Ser Arg Asn Asn Asn Glu
 275 280 285
 Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys Gly Asp Glu Phe Cys
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 325 330 335
 Gln Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu
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 Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu
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 Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile
 370 375 380
 Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu Gln Gly Leu Phe
 385 390 395 400
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 Arg Arg His Leu Cys Cys Gly Arg Phe Arg Leu Ala Asp Asn Ser Asp
 420 425 430
 Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys Ser Ser Asp Asn Leu
 435 440 445
 Gly Lys Ser Leu Ser Ser Ser Ile Gly Ser Asn Ser Thr Tyr Leu
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 Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr Phe Lys Arg Asn Ser
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Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
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Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
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35 40 45
Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
50 55 60
Gin Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln
65 70 75 80
Ile Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr
85 90 95
Asp Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly
100 105 110
Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ala Asn Glu Met His
115 120 125
Val Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala
130 135 140
Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu
145 150 155 160
Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser
165 170 175
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180 185 190
Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser
195 200 205
Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu
210 215 220
Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys
225 230 235 240
Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val
245 250 255
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260 265 270
Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn
275 280 285
Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys
290 295 300
Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys
305 310 315 320
Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp
325 330 335
Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser
340 345 350
Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu
355 360 365
Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Asp Gly Ile Ile Tyr
370 375 380
Arg Ile Ser Val Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys
385 390 395 400

Val Gln Ser Lys Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp
 405 410 415
 Asn Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly
 420 425 430
 Glu Asp Lys Ile Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu
 435 440 445
 Val Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu
 450 455 460
 Glu Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu
 465 470 475 480
 Asp Glu Gly Leu Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His
 485 490 495
 Cys Leu Ala Met Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln
 500 505 510
 Pro Ser Glu Tyr Val Leu Pro Cys Pro Asp Lys Pro Gly Phe Ser Ala
 515 520 525
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 580 585 590
 Glu Asn Ile Asp Ile Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser
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 Ala Leu Lys Thr Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser
 625 630 635 640
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 Ser Leu Leu Pro Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu
 660 665 670
 Pro Ser Asn Asn Glu Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln
 675 680 685
 Val Asp Pro Leu Ala Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn
 690 695 700
 Leu Ser Pro Glu Asp Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe
 705 710 715 720
 Phe Asn Lys Thr Gly Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr
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 740 745 750
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 Glu Val His His Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys
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 Thr Lys Val Leu Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala
 835 840 845

Ile Phe Ser Ala Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Lys Leu
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<211> 1193

<212> PRT

<213> homo sapiens

<400> 36

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Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser	
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Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln	
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Ile Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr	
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Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His	
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Val Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala	
130 135 140	
Ser Tyr Ile Arg Val Ala Val Ser Leu Arg Asn Gln Lys Val Ile Leu	
145 150 155 160	
Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser	
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Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val	
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Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser	
195 200 205	
Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu	
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Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val	
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Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr	
260 265 270	
Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn	
275 280 285	
Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys	
290 295 300	
Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys	
305 310 315 320	
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Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser	
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Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu	
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Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Asp Gly Ile Ile Tyr
 370 375 380
 Arg Ile Ser Val Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys
 385 390 395 400
 Val Gln Ser Lys Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp
 405 410 415
 Asn Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly
 420 425 430
 Glu Asp Lys Ile Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu
 435 440 445
 Val Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu
 450 455 460
 Glu Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu
 465 470 475 480
 Asp Glu Gly Leu Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His
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 Cys Leu Ala Met Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln
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 Pro Ser Glu Tyr Val Leu Pro Cys Pro Asp Lys Pro Gly Phe Ser Ala
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 Gly Pro Val Asp Ile Ser Asn Cys Leu Lys Glu Ala Asn Glu Val Ala
 545 550 555 560
 Asn Gln Ile Leu Asn Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala
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 580 585 590
 Glu Asn Ile Asp Ile Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser
 595 600 605
 Asn Ile Leu Ser Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu
 610 615 620
 Ala Leu Lys Thr Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser
 625 630 635 640
 Thr Ser His Val Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser
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 Ser Leu Leu Pro Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu
 660 665 670
 Pro Ser Asn Asn Glu Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln
 675 680 685
 Val Asp Pro Leu Ala Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn
 690 695 700
 Leu Ser Pro Glu Asp Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe
 705 710 715 720
 Phe Asn Lys Thr Gly Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr
 725 730 735
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 740 745 750
 Asn Leu Lys Asp Pro Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln
 755 760 765
 Glu Val His His Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys
 770 775 780
 Ser Phe Gly Gly Trp Asn Thr Ser Gly Cys Val Ala His Arg Asp Ser
 785 790 795 800
 Asp Ala Ser Glu Thr Val Cys Leu Cys Asn His Phe Thr His Phe Gly
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Val Leu Met Asp Leu Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn
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 Thr Lys Val Leu Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala
 835 840 845
 Ile Phe Ser Ala Ala Thr Leu Leu Thr Tyr Val Ala Phe Glu Lys Leu
 850 855 860
 Arg Arg Asp Tyr Pro Ser Lys Ile Leu Met Asn Leu Ser Thr Ala Leu
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 Leu Phe Leu Asn Leu Leu Phe Leu Leu Asp Gly Trp Ile Thr Ser Phe
 885 890 895
 Asn Val Asp Gly Leu Cys Ile Ala Val Ala Val Leu Leu His Phe Phe
 900 905 910
 Leu Leu Ala Thr Phe Thr Trp Met Gly Leu Glu Ala Ile His Met Tyr
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 Val Leu Ala Ser Arg Asn Asn Asn Gln Val Tyr Gly Lys Glu Ser Tyr
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 Gly Lys Glu Lys Gly Asp Glu Phe Cys Trp Ile Gln Asp Pro Val Ile
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<211> 2073

<212> DNA

<213> homo sapiens

<400> 37

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ata	acca	actt	ga	atgg	cc	acc	gtt	300
ctt	gata	at	tt	gag	cc	aa	agg	360
aact	caag	tg	tt	gag	ct	atc	atc	420
g	ttt	caat	g	ttt	ca	atc	atc	480
cccc	agac	at	tt	gat	cc	atc	tat	540
agt	gtt	tc	act	ctg	tga	aa	ggc	600
g	ttt	cct	c	act	aa	ttt	atc	660
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tt	gg	at	tt	ttt	ttt	ttt	ttt	1080
at	ccc	ct	tt	ttt	ttt	ttt	ttt	1140
gg	att	at	tt	ttt	ttt	ttt	ttt	1200
gt	ac	ag	tt	ttt	ttt	ttt	ttt	1260
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tt	gg	ttt	ttt	ttt	ttt	ttt	ttt	1500
tt	gg	ttt	ttt	ttt	ttt	ttt	ttt	1560
cc	ca	ca	ttt	ttt	ttt	ttt	ttt	1620
gt	aa	cc	ttt	ttt	ttt	ttt	ttt	1680
aa	act	ttt	ttt	ttt	ttt	ttt	ttt	1740
tt	tt	ttt	ttt	ttt	ttt	ttt	ttt	1800
tt	tt	ttt	ttt	ttt	ttt	ttt	ttt	1860
tc	at	tt	ttt	ttt	ttt	ttt	ttt	1920
tc	at	tt	ttt	ttt	ttt	ttt	ttt	1980
ac	at	tt	ttt	ttt	ttt	ttt	ttt	2040
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<211> 690

<212> PRT

<213> homo sapiens

<400> 38

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							20		25			30			
Ser	Ala	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
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Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
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Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
							65		70			75			80
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
							85		90			95			
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
							100		105			110			
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His

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Pro Gln Thr Ser Asp Ala Tyr Gln Val Ser Val Ala Lys Ser Ile Ser		
165	170	175
Ile Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val		
180	185	190
Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser		
195	200	205
Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu		
210	215	220
Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys		
225	230	235
Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val		
245	250	255
Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr		
250	265	270
Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn		
275	280	285
Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys		
290	295	300
Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys		
305	310	315
Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp		
325	330	335
Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser		
340	345	350
Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu		
355	360	365
Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Asp Gly Ile Ile Tyr		
370	375	380
Arg Ile Ser Val Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys		
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Val Gln Ser Lys Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp		
405	410	415
Asn Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly		
420	425	430
Glu Asp Lys Ile Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu		
435	440	445
Val Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu		
450	455	460
Glu Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu		
465	470	475
Asp Glu Gly Leu Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His		
485	490	495
Cys Leu Ala Met Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln		
500	505	510
Pro Ser Glu Tyr Val Leu Pro Cys Pro Asp Lys Pro Gly Phe Ser Ala		
515	520	525
Ser Arg Ile Cys Phe Tyr Asn Ala Thr Asn Pro Leu Val Thr Tyr Trp		
530	535	540
Gly Pro Val Asp Ile Ser Asn Cys Leu Lys Glu Ala Asn Glu Val Ala		
545	550	555
Asn Gln Ile Leu Asn Leu Thr Ala Asp Gly Gln Asn Leu Thr Ser Ala		

565	570	575
Asn Ile Thr Asn Ile Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu		
580	585	590
Glu Asn Ile Asp Ile Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser		
595	600	605
Asn Ile Leu Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu		
610	615	620
Ala Leu Lys Thr Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser		
625	630	640
Thr Ser His Val Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser		
645	650	655
Ser Leu Leu Pro Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu		
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690		

<210> 39

<211> 3255

<212> DNA

<213> homo sapiens

<400> 39

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Ile Leu Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Glu Ala			
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Leu Lys Thr Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser Thr			
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Ser His Val Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser Ser			
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Leu Leu Pro Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu Pro			
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Ser Asn Asn Glu Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln Val			
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Asp Pro Leu Ala Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn Leu			
690	695	700	
Ser Pro Glu Asp Ser Val Leu Val Arg Arg Ala Gln Phe Thr Phe Phe			
705	710	715	720
Asn Lys Thr Gly Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr Leu			
725	730	735	
Val Ser Tyr Val Met Ala Cys Ser Ile Gly Asn Ile Thr Ile Gln Asn			
740	745	750	

Leu Lys Asp Pro Val Gln Ile Lys Ile Lys His Thr Arg Thr Gln Glu
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 Val His His Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys Ser
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 Ala Ser Glu Thr Val Cys Leu Cys Asn His Phe Thr His Phe Gly Val
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 Leu Met Asp Leu Pro Arg Ser Ala Ser Gln Leu Asp Ala Arg Asn Thr
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 Lys Val Leu Thr Phe Ile Ser Tyr Ile Gly Cys Gly Ile Ser Ala Ile
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 Ile Pro Val His Gln Val Ile Asp Lys Val Lys Gly Tyr Cys Asn Ala
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<211> 3579

<212> DNA

<213> homo sapiens

<400> 43

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<310> 44

<311> 1192

<312> PRT

<313> homo sapiens

<400> 44

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Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro	Ser
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Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser	Gln
						50			55			60			
Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln	Ile
						65			70			75			80
Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr	Asp
						85			90			95			
Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly	Ala
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Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His	Val
						115			120			125			
Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala	Ser
						130			135			140			
Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu	Pro
						145			150			155			160
Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser	Ile
						165			170			175			
Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val	Gly
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His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser	Phe
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Thr	Gln	Leu	Leu	Ser	Phe	Gly	Lys	Ala	Lys	Ser	Gly	Tyr	Phe	Leu	Ser
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Ile	Ser	Asp	Ser	Lys	Cys	Leu	Leu	Asn	Asn	Ala	Leu	Pro	Val	Lys	Glu
						225			230			235			240
Lys	Glu	Asp	Ile	Phe	Ala	Glu	Ser	Phe	Glu	Gln	Leu	Cys	Leu	Val	Trp
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Asn	Asn	Ser	Leu	Gly	Ser	Ile	Gly	Val	Asn	Phe	Lys	Arg	Asn	Tyr	Glu
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 Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys Gly
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 Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys Ile
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 Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp Gln
 325 330 335
 Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser Asn
 340 345 350
 Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu Ala
 355 360 365
 Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Asp Gly Ile Ile Tyr Arg
 370 375 380
 Ile Ser Val Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val
 385 390 395 400
 Gln Ser Lys Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn
 405 410 415
 Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu
 420 425 430
 Asp Lys Ile Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val
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 Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu Glu
 450 455 460
 Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu Asp
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 Glu Gly Leu Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His Cys
 485 490 495
 Leu Ala Met Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln Pro
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 515 520 525
 Arg Ile Cys Phe Tyr Asn Ala Thr Asn Pro Leu Val Thr Tyr Trp Gly
 530 535 540
 Pro Val Asp Ile Ser Asn Cys Leu Lys Glu Ala Asn Glu Val Ala Asn
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 Ile Thr Asn Ile Val Glu Gln Val Lys Arg Ile Val Asn Lys Glu Glu
 580 585 590
 Asn Ile Asp Ile Thr Leu Gly Ser Thr Leu Met Asn Ile Phe Ser Asn
 595 600 605
 Ile Leu Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu Ala
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 Leu Lys Thr Ile Asp Glu Leu Ala Phe Lys Ile Asp Leu Asn Ser Thr
 625 630 635 640
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 645 650 655
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 Ser Asn Asn Glu Ser Tyr Phe Gln Met Asp Phe Glu Ser Gly Gln Val
 675 680 685
 Asp Pro Leu Ala Ser Val Ile Leu Pro Pro Asn Leu Leu Glu Asn Leu
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Asn Lys Thr Gly Leu Phe Gln Asp Val Gly Pro Gln Arg Lys Thr Leu
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 Val His His Pro Ile Cys Ala Phe Trp Asp Leu Asn Lys Asn Lys Ser
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 Ile Gly Ser Asn Ser Thr Tyr Leu Thr Ser Lys Ser Lys Ser Ser Ser
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 Thr Thr Tyr Phe Lys Arg Asn Ser His Thr Asp Asn Val Ser Tyr Glu
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 Val Leu Val Lys Thr Gly Pro Cys
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<211> 2070

<212> DNA

<213> homo sapiens

<400> 45

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<211> 689

<212> PRT

<213> homo sapiens

<400> 46

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Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln Ile		
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Thr Phe Asn Asp Phe Asp Ile Glu Glu Ala Pro Asn Cys Ile Tyr Asp		
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Ser Leu Ser Leu Asp Asn Gly Glu Ser Gln Thr Lys Phe Cys Gly Ala		
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Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His Val		
115	120	125
Ser Phe Ser Ser Asp Phe Ser Ile Gln Lys Lys Gly Phe Asn Ala Ser		
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Pro Glu Leu Ser Ala Phe Thr Leu Cys Phe Glu Ala Thr Lys Val Gly		
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His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser Phe		
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Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu Ser		
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225	230	235
Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val Trp		
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Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr Glu		
260	265	270
Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn Gly		
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Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys Gly		
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Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys Ile		
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Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp Gln		
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Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser Asn		
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Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu Ala		
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Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Asp Gly Ile Ile Tyr Arg		
370	375	380
Ile Ser Val Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys Val		
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Gln Ser Lys Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp Asn		
405	410	415
Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly Glu		
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Asp Lys Ile Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu Val		
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Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu Glu		
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Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu Asp		

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His	Thr	Val	Asn
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Pro	Ser	Ile	Gln
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Ser	Glu	Tyr	Val
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Pro	Asp	Lys	Pro
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Phe	Tyr	Asn	Ala
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Leu	Val	Val	Thr
Thr	Tyr	Trp	Gly
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Gln	Val	Lys	Arg
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<213> homo sapiens

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<210> 50

<211> 1222

<212> PRT

<213> homo sapiens

<400> 50

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His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
							35			40			45		
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
							50			55			60		
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
							65			70			75		80
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
							85			90			95		
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
							100			105			110		
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
							115			120			125		
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
							130			135			140		
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
							145			150			155		160
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
							165			170			175		
Ile	Pro	Glu	Leu	Ser	Ala	Phe	Thr	Leu	Cys	Phe	Glu	Ala	Thr	Lys	Val
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Gly	His	Glu	Asp	Ser	Asp	Trp	Thr	Ala	Phe	Ser	Tyr	Ser	Asn	Ala	Ser
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 Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys
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 Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val
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 Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr
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 Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn
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 Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys
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 Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys
 305 310 315 320
 Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp
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 Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser
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 Asn Leu Ser Cys Gly Ser Tyr Leu Ile Pro Leu Pro Ala Ala Glu Leu
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 Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Asp Gly Ile Ile Tyr
 370 375 380
 Arg Ile Ser Val Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys
 385 390 395 400
 Val Gln Ser Lys Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp
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 Asn Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly
 420 425 430
 Glu Asp Lys Ile Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu
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 Val Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu
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 Glu Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu
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 Cys Leu Ala Met Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln
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 Ser Arg Ile Cys Phe Tyr Asn Ala Thr Asn Pro Leu Val Thr Tyr Trp
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 Gly Pro Val Asp Ile Ser Asn Cys Leu Lys Glu Ala Asn Glu Val Ala
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 690 695 700
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 705 710 715 720
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 Leu Val Ser Tyr Val Met Ala Cys Ser Ile Gly Asn Ile Thr Ile Gin
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 785 790 795 800
 Asp Ala Ser Glu Thr Val Cys Leu Cys Asn His Phe Thr His Phe Gly
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 835 840 845
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 Lys Phe Cys Ile Ile Gly Trp Gly Leu Pro Ala Leu Val Val Ser Val
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 1075 1080 1085
 Met Lys Glu Asn Val Gln Lys Gln Trp Arg Arg His Leu Cys Cys Gly
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Arg Phe Arg Leu Ala Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn
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 Ser Thr Thr Tyr Phe Lys Arg Asn Ser His Thr Asp Ser Ala Ser Met
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<212> DNA

<213> homo sapiens

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<210> 52
<211> 1193
<212> PRT
<213> homo sapiens

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			20		25		30								
His	Ser	Val	Trp	Gly	Cys	Ala	Asn	Cys	Arg	Val	Val	Leu	Ser	Asn	Pro
			35		40		45								
Ser	Gly	Thr	Phe	Thr	Ser	Pro	Cys	Tyr	Pro	Asn	Asp	Tyr	Pro	Asn	Ser
			50		55		60								
Gln	Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln
			65		70		75				80				
Ile	Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr
			85		90		95								
Asp	Ser	Leu	Ser	Leu	Asp	Asn	Gly	Glu	Ser	Gln	Thr	Lys	Phe	Cys	Gly
			100		105		110								
Ala	Thr	Ala	Lys	Gly	Leu	Ser	Phe	Asn	Ser	Ser	Ala	Asn	Glu	Met	His
			115		120		125								
Val	Ser	Phe	Ser	Ser	Asp	Phe	Ser	Ile	Gln	Lys	Lys	Gly	Phe	Asn	Ala
			130		135		140								
Ser	Tyr	Ile	Arg	Val	Ala	Val	Ser	Leu	Arg	Asn	Gln	Lys	Val	Ile	Leu
			145		150		155				160				
Pro	Gln	Thr	Ser	Asp	Ala	Tyr	Gln	Val	Ser	Val	Ala	Lys	Ser	Ile	Ser
			165		170		175								

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 Gly His Glu Asp Ser Asp Trp Thr Ala Phe Ser Tyr Ser Asn Ala Ser
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 Phe Thr Gln Leu Leu Ser Phe Gly Lys Ala Lys Ser Gly Tyr Phe Leu
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 Ser Ile Ser Asp Ser Lys Cys Leu Leu Asn Asn Ala Leu Pro Val Lys
 225 230 235 240
 Glu Lys Glu Asp Ile Phe Ala Glu Ser Phe Glu Gln Leu Cys Leu Val
 245 250 255
 Trp Asn Asn Ser Leu Gly Ser Ile Gly Val Asn Phe Lys Arg Asn Tyr
 260 265 270
 Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn
 275 280 285
 Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys
 290 295 300
 Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys
 305 310 315 320
 Ile Leu Ser Asn Leu Ser Cys Asn Val Lys Gly Asn Val Val Asp Trp
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 Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser
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 Ala Ser Cys Ala Asp Leu Gly Thr Leu Cys Gln Asp Gly Ile Ile Tyr
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 Arg Ile Ser Val Val Ile Gln Asn Ile Leu Arg His Pro Glu Val Lys
 385 390 395 400
 Val Gln Ser Lys Val Ala Glu Trp Leu Asn Ser Thr Phe Gln Asn Trp
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 Asn Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly
 420 425 430
 Glu Asp Lys Ile Lys Val Lys Arg Ser Leu Glu Asp Glu Pro Arg Leu
 435 440 445
 Val Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu
 450 455 460
 Glu Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu
 465 470 475 480
 Asp Glu Gly Leu Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His
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 Cys Leu Ala Met Glu Glu Pro Lys Gly Tyr Tyr Trp Pro Ser Ile Gln
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 Asn Ile Leu Ser Ser Ser Asp Ser Asp Leu Leu Glu Ser Ser Ser Glu
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 Arg Phe Arg Leu Ala Asp Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn
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<211> 2073

<212> DNA

<213> homo sapiens

<400> 53

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ataacattt	aacgacttt	catatggaaa	gtccccaatt	gcatttatga	ctcattatcc	310
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2073

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Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
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Gln Ala Cys Met Trp Thr Leu Arg Ala Pro Thr Gly Tyr Ile Ile Gln
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Ala Thr Ala Lys Gly Leu Ser Phe Asn Ser Ser Ala Asn Glu Met His
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Glu Thr Val Pro Cys Asp Ser Thr Ile Ser Lys Val Ile Pro Gly Asn
275 280 285
Gly Lys Leu Leu Leu Gly Ser Asn Gln Asn Glu Ile Val Ser Leu Lys
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Gly Asp Ile Tyr Asn Phe Arg Leu Trp Asn Phe Thr Met Asn Ala Lys
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Gln Asn Asp Phe Trp Asn Ile Pro Asn Leu Ala Leu Lys Ala Glu Ser
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Asn Tyr Thr Val Tyr Val Val Asn Ile Ser Phe His Leu Ser Ala Gly		
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Val Leu Trp Ala Leu Leu Val Tyr Asn Ala Thr Asn Asn Thr Asn Leu		
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Glu Gly Lys Ile Ile Gln Gln Lys Leu Leu Lys Asn Asn Glu Ser Leu		
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Asp Glu Gly Leu Arg Leu His Thr Val Asn Val Arg Gln Leu Gly His		
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Cys Leu Ala Met Glu Glu Pro Lys Gly Tyr Trp Pro Ser Ile Gln		
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Thr Ser His Val Asn Ile Thr Thr Arg Asn Leu Ala Leu Ser Val Ser		
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Ser Leu Leu Pro Gly Thr Asn Ala Ile Ser Asn Phe Ser Ile Gly Leu		
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 Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
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Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu	Gly	Met	Thr	Trp	Gly	Phe	Ala
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<311> 3579

<212> DNA

<313> homo sapiens

<400> 57

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<211> 1192

<212> PRT

<213> homo sapiens

<400> 58

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Ala	Cys	Met	Trp	Thr	Leu	Arg	Ala	Pro	Thr	Gly	Tyr	Ile	Ile	Gln	Ile
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Thr	Phe	Asn	Asp	Phe	Asp	Ile	Glu	Glu	Ala	Pro	Asn	Cys	Ile	Tyr	Asp
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Asn	Lys	Thr	Gly	Leu	Phe	Gln	Asp	Val	Gly	Pro	Gln	Arg	Lys	Thr	Leu
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Sequence Comparison A

RESULT 8
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LOCUS T71087 520 bp mRNA linear EST 01-MAR-1995
DEFINITION yc50d03.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:84101 5', mRNA sequence.
ACCESSION T71087
VERSION T71087.1 GI:685608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
, M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
, Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlffing,T.,
Scheellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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High quality sequence stops: 314 Source: IMAGE Consortium, LLNL This
clone is available royalty-free through LLNL ; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
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dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb, Uni-ZAP XR Vector; -5' adaptor sequence 5'
GAATTCTGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTT 3'
BASE COUNT 138 a 92 c 122 g 162 t 6 others
ORIGIN

Query Match 6.0%; Score 225.4, DB 10; Length 520;
Best Local Similarity 99.6%; Pred. No. 2 8e-47;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 2 TTTTCTAATATCTTAAGCAGTCAGACAGTGACTTGCTTGAGTCATCTTCTGAAGCTTAA 61
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Db 62 AAAACAATTGTATGAATTGGCCTTCAAGATAGACCTAAATAGCACATCACATGTGAATATT 121

Qy 2023 acaactcgaaacttggcttcagcgtatcatccctgttaccaggacaaatgcaattca 2082
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Db 122 ACAACTCGGAACTTGGCTCTCAGCGTATCATCCCTGTTACCAGGGACAAATGCAATTCA 181

Qy 2083 aattttagcattggcttccaaggcaataatgaatcgatttccagat 2129
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Db 182 AATTTTAGCATTGGCTTCCAAGCAATAATGAATCGTATTCAGGT 228

Results 09658283

RESULT 4
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LOCUS AA796299 472 bp mRNA linear EST 09-FEB-1998
DEFINITION vs94b12.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1153919 5', mRNA sequence
ACCESSION AA796299
VERSION AA796299.1 GI 2859254
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 472)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:627127
Seq primer: -28m13 rev2 ET from Amersham.
FEATURES Location/Qualifiers
source 1. .472
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1153919"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACGAATCTGAAGTGGGAGCGGCCGCCCCCTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCTGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins. "
BASE COUNT 98 a 123 c 111 g 140 t
ORIGIN

Query Match 9.2%; Score 345, DB 9; Length 472;
Best Local Similarity 85.7%; Pred. No. 2.5e-78;
Matches 395; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

Qy 2384 ctcaggaagtgcataccatctgtgccttctggatctgaacaaaacaaaagtttg 2443
Db 13 CACAGGAAGTCGATCATCCTATCTGTGCCTCTGGATATGAACAAAACAAAAGTTTCG 72
Qy 2444 gagatggaaacacgtcaggatgttgtgcacacagagattcagatgcaagtgagacagtct 2503
Db 73 GGGGGTGGAACAC-TCAGGATGTGTTGCCACTCTGATTTGGACGCTGGTGAGACCATT 131
Qy 2504 gcctgttaaccacttcacacactttggagttctgatggacccccaagaagtgcctcac 2563

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Db    132 GTCTGTGCAGCCACTTCACTTGAGTTCTGATGGATCTTCAAGGAGTGCCTCAC 191
Qy    2564 agtttagatgcaagaaaactaaagtccacttcatcagctatattgggtgtgaaatat 2623
Db    192 AAATAGATGGAAGAACACAAAAGTCCTCACGTTCATTACCTATATTGGGTGCGGAATAT 251
Qy    2624 ctgcatttttcagcagcaacttcctgacatatgttgcatttgagaaattgcgaagg 2683
Db    252 CTGCCATTTCAGCTGCAACTTCCTGACATATGTTGCTTGAGAAGCTGCGCAGGG 311
Qy    2684 attatccctccaaatcttgcatttgcacagccctgtgttgcatttcctgcatttgc 2743
Db    312 ATTATCCCTCCAAAATCCTGATGAATCTGAGCTCGGCCTTGCTCTCCTGAATCTCATCT 371
Qy    2744 tcctccatggatggctggatcaccccttcataatgtggatggactttgcattgttgc 2803
Db    372 TCCTCCTGGATGGCTGGGTCACTTCCTTGGCGTGGCTGGACTCTGCACGGCTGGCTG 431
Qy    2804 tcctgtgcatttcttcatttgcaccccttgcatttgcatttgc 2844
Db    432 CCCTGTTGCACTTCCTGGCTACCTCACCTGGATG 472

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RESULT 8
T71087

LOCUS T71087 520 bp mRNA linear EST 01-MAR-1995
DEFINITION yc50d03.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:84101 5', mRNA sequence.

ACCESSION T71087
VERSION T71087.1 GI:685608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 520)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 592
High quality sequence stops: 314 Source IMAGE Consortium, LLNL This
clone is available royalty-free through LLNL ; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
Insert Length: 592 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 314.

FEATURES Location/Qualifiers
source 1..520
/organism="Homo sapiens"
/db_xref="GDB:501158"
/db_xref="taxon:9606"
/clone="IMAGE:84101"
/clone_lib="Stratagene liver (#937224)"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI

; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence 5'
GAATTCTGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3'"
BASE COUNT 138 a 92 c 122 g 162 t 6 others
ORIGIN

Query Match 6.0%; Score 225.4; DB 10; Length 520;
Best Local Similarity 99.6%; Pred. No. 2.8e-47;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1903 ttttctaataatcttaaggcagttcagacagtgacttgcttgagtcatcttctgaagcttta 1962
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 TTTTCTAATATCTTAAGCAGTTCAAGACAGTGACTTGCTTGAGTCATCTTCTGAAGCTTTA 61

Qy 1963 aaaacaattgtatggccttcagaatagacactaaatagcacatcacatgtgaatatt 2022
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 AAAACAATTGATGAATTGGCCTTCAAGATAGACACTAAATAGCACATCACATGTGAATATT 121

Qy 2023 acaactcgaaacttggctctcagcgtatcatccctgttaccaggggacaaatgcaattca 2082
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 ACAACTCGGAACCTTGGCTCTCAGCGTATCATCCCTGTTACCAGGGACAAATGCAATTCA 181

Qy 2083 aatttagcattggcttccaaggcaataatgaatcgatattccagat 2129
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 AATTAGCATTGGCTTCCAAGCAATAATGAATCGTATTCAGGT 228